

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/568,763
Source: IFWP
Date Processed by STIC: 03/07/2006

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/568,763

CRF Edit Date: 03/07/2006
Edited by: DA

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

/ Deleted: invalid beginning/end-of-file text ; page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



IFWP

RAW SEQUENCE LISTING

DATE: 03/07/2006

PATENT APPLICATION: US/10/568,763

TIME: 09:53:32

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\03072006\J568763.raw

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3 <110> APPLICANT: Bayer AG, BHC
W--> 4 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
Kallikrein 9
W--> 5 (KLK9)
W--> 6 <130> FILE REFERENCE: Le A 36 871
C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/568,763
C--> 7 <141> CURRENT FILING DATE: 2006-02-21
W--> 7 <160> NUMBER OF SEQ ID: 5
8 <170> SOFTWARE: PatentIn version 3.1
W--> 9 <210> SEQ ID NO: 1
10 <211> LENGTH: 753
11 <212> TYPE: DNA
12 <213> ORGANISM: Homo sapiens
W--> 13 <400> SEQUENCE: 1
14 atgaagctgg gactcctctg tgctctgctc tctctgctgg cagggcatgg ctgggcagac 60
15 acccgtagca tgggggcca ggaatgtcgc cccaactccc agccttggca ggccggcctc 120
16 ttccacctta ctcggtctt ctgtggggcg accctcatca gtgaccgctg gctgtctaca 180
17 gctgcccact gccgcaagcc gtatctgtgg gtccgccttg gagagcacca cctctggaaa 240
18 tgggaggggc cggagcagct gttccgggtt acggacttct tccccaccc tggcttcaac 300
19 aaggacctca gcgccaatga ccacaatgat gacatcatgc tgatccgcct gccagggcag 360
20 gcacgtctga gtccgtctgt gcagcccctc aacctcagcc agacctgtgt ctcccaggc 420
21 atgcagtgtc tcattctcagg ctggggggcc gtgtccagcc ccaaggcgct gtttcagtc 480
22 aactgtcagt gtgccaacat cagcatcctg gagaacaaac tctgtcactg ggcataccct 540
23 ggacacatct cggacagcat gctctgtgcg ggcctgtggg agggggggccg aggttcctgc 600
24 cagggtgact ctggggggcc cctggtttgc aatggaaacct tggcaggcgt ggtgtctggg 660
25 ggtgtgagc cctgtctccag accccggcgc cccgcagtct acaccagcgt atgccactac 720
26 cttgactgga tccaagaaat catggagaac tga 753
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 250
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
W--> 31 <400> SEQUENCE: 2
32 Met Lys Leu Gly Leu Leu Cys Ala Leu Leu Ser Leu Leu Ala Gly His
33 1 5 10 15
34 Gly Trp Ala Asp Thr Arg Ala Ile Gly Ala Glu Glu Cys Arg Pro Asn
35 20 25 30
36 Ser Gln Pro Trp Gln Ala Gly Leu Phe His Leu Thr Arg Leu Phe Cys
37 35 40 45
38 Gly Ala Thr Leu Ile Ser Asp Arg Trp Leu Leu Thr Ala Ala His Cys
39 50 55 60
40 Arg Lys Pro Tyr Leu Trp Val Arg Leu Gly Glu His His Leu Trp Lys
41 65 70 75 80
42 Trp Glu Gly Pro Glu Gln Leu Phe Arg Val Thr Asp Phe Phe Pro His
43 85 90 95

```

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44 Pro Gly Phe Asn Lys Asp Leu Ser Ala Asn Asp His Asn Asp Asp Ile
45           100           105           110
46 Met Leu Ile Arg Leu Pro Arg Gln Ala Arg Leu Ser Pro Ala Val Gln
47           115           120           125
48 Pro Leu Asn Leu Ser Gln Thr Cys Val Ser Pro Gly Met Gln Cys Leu
49           130           135           140
50 Ile Ser Gly Trp Gly Ala Val Ser Ser Pro Lys Ala Leu Phe Pro Val
51 145           150           155           160
52 Thr Leu Gln Cys Ala Asn Ile Ser Ile Leu Glu Asn Lys Leu Cys His
53           165           170           175
54 Trp Ala Tyr Pro Gly His Ile Ser Asp Ser Met Leu Cys Ala Gly Leu
55           180           185           190
56 Trp Glu Gly Gly Arg Gly Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu
57           195           200           205
58 Val Cys Asn Gly Thr Leu Ala Gly Val Val Ser Gly Gly Ala Glu Pro
59           210           215           220
60 Cys Ser Arg Pro Arg Arg Pro Ala Val Tyr Thr Ser Val Cys His Tyr
61 225           230           235           240
62 Leu Asp Trp Ile Gln Glu Ile Met Glu Asn
63           245           250

```

64 <210> SEQ ID NO: 3

65 <211> LENGTH: 19

66 <212> TYPE: DNA

67 <213> ORGANISM: artificial sequence

W--> 68 <220> FEATURE:

69 <223> OTHER INFORMATION: forward primer

W--> 70 <400> SEQUENCE: 3

71 gcgctgtttc cagtcacac

19

72 <210> SEQ ID NO: 4

73 <211> LENGTH: 21

74 <212> TYPE: DNA

75 <213> ORGANISM: artificial sequence

W--> 76 <220> FEATURE:

77 <223> OTHER INFORMATION: reverse primer

W--> 78 <400> SEQUENCE: 4

79 gccagtgac agagtttggt c

21

80 <210> SEQ ID NO: 5

81 <211> LENGTH: 24

82 <212> TYPE: DNA

83 <213> ORGANISM: artificial sequence

W--> 84 <220> FEATURE:

85 <223> OTHER INFORMATION: probe

W--> 86 <400> SEQUENCE: 5

87 cagtgtgccacatcagcat cctg

24

VERIFICATION SUMMARY

DATE: 03/07/2006

PATENT APPLICATION: US/10/568,763

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Input Set : A:\pto.da.txt

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L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:7 M:283 W: Missing Blank Line separator, <160> field identifier
L:9 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <400> field identifier
L:31 M:283 W: Missing Blank Line separator, <400> field identifier
L:68 M:283 W: Missing Blank Line separator, <220> field identifier
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:76 M:283 W: Missing Blank Line separator, <220> field identifier
L:78 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:283 W: Missing Blank Line separator, <220> field identifier
L:86 M:283 W: Missing Blank Line separator, <400> field identifier

**Raw Sequence Listing before editing
(for reference only)**



IFWP

RAW SEQUENCE LISTING

DATE: 03/07/2006

PATENT APPLICATION: US/10/568,763

TIME: 09:05:56

Input Set : A:\ptol.da.txt

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3 <110> APPLICANT: Bayer AG, BHC
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W--> 5 (KLK9)

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W--> 9 <210> SEQ ID NO: 1

10 <211> LENGTH: 753

11 <212> TYPE: DNA

12 <213> ORGANISM: Homo sapiens

W--> 13 <400> SEQUENCE: 1

14	atgaagctgg gactcctctg tgctctgctc tctctgctgg cagggcatgg ctgggcagac	60
15	accctgtcca tcggggccga ggaatgtcgc cccaactccc agccttggca ggccggcctc	120
16	ttccacctta ctcggtcttt ctgtggggcg accctcatca gtgaccgctg gctgctcaca	180
17	gctgcccact gccgcaagcc gtatctgtgg gtccgccttg gagagcacca cctctggaaa	240
18	tgggagggtc cggagcagct gttccgggtt acggacttct tccccaccc tggcttcaac	300
19	aaggacctca gcgccaatga ccacaatgat gacatcatgc tgatccgcct gcccaggcag	360
20	gcacgtctga gtcctgtgtg gcagcccctc aacctcagcc agacctgtgt ctcccaggc	420
21	atgcagtgtc tcatctcagg ctggggggcc gtgtccagcc ccaaggcgct gtttccagtc	480
22	acactgcagt gtgccaacat cagcatcctg gagaacaaac tctgtcactg ggcataacct	540
23	ggacacatct cggacagcat gctctgtgcy ggctgtggg agggggggccg aggttctctgc	600
24	caggggtgact ctggggggccc cctggtttgc aatggaacct tggcaggcgt ggtgtctggg	660
25	ggtgtctgagc cctgtctccag accccggcgc cccgcagtct acaccagcgt atgccactac	720
26	cttgactgga tccaagaaat catggagaac tga	753

27 <210> SEQ ID NO: 2

28 <211> LENGTH: 250

29 <212> TYPE: PRT

30 <213> ORGANISM: Homo sapiens

W--> 31 <400> SEQUENCE: 2

32	Met Lys Leu Gly Leu Leu Cys Ala Leu Leu Ser Leu Leu Ala Gly His	
33	1 5 10 15	
34	Gly Trp Ala Asp Thr Arg Ala Ile Gly Ala Glu Glu Cys Arg Pro Asn	
35	20 25 30	
36	Ser Gln Pro Trp Gln Ala Gly Leu Phe His Leu Thr Arg Leu Phe Cys	
37	35 40 45	
38	Gly Ala Thr Leu Ile Ser Asp Arg Trp Leu Leu Thr Ala Ala His Cys	
39	50 55 60	
40	Arg Lys Pro Tyr Leu Trp Val Arg Leu Gly Glu His His Leu Trp Lys	
41	65 70 75 80	
42	Trp Glu Gly Pro Glu Gln Leu Phe Arg Val Thr Asp Phe Phe Pro His	
43	85 90 95	

Does Not Comply
 Corrected Diskette Needed

(p3-2)

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49           130           135           140
50 Ile Ser Gly Trp Gly Ala Val Ser Ser Pro Lys Ala Leu Phe Pro Val
51 145           150           155           160
52 Thr Leu Gln Cys Ala Asn Ile Ser Ile Leu Glu Asn Lys Leu Cys His
53           165           170           175
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W--> 86 <400> SEQUENCE: 5

87 cagtgtgccacacacagcat cctg

24

W--> 89 Le A 36 871-Foreign Countries

W--> 92 - 3 -

W--> 96 Le A 36 871-Foreign Countries

W--> 99 - 1 -

VERIFICATION SUMMARY

DATE: 03/07/2006

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L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:76 M:283 W: Missing Blank Line separator, <220> field identifier
L:78 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:283 W: Missing Blank Line separator, <220> field identifier
L:86 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:96 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5